

#4

SEQUENCE LISTING

<110> CHOE, Sunghwa
FELDMANN A., Kenneth

<120> Dwf5 MUTANTS

<130> 2225-0020 / 91020.002

<140> 09/817,774

<141> 2001-03-26

<150> 60/192,202

<151> 2000-03-27

<160> 45

<170> PatentIn Ver. 2.0

<210> 1

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DW5_FF

<400> 1

gtgtgagtaa tttagggtcaa cacagatca

29

<210> 2

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DW5_LR

<400> 2

ggctcggtct tttgatgatt ccaacggt

28

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DW5_2F

<400> 3

tgtggttaacc taataattga cttctatt

28

<210> 4
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: DW5_2R

 <400> 4
 ggagaagtgt agacagaagg cacccacact 30

 <210> 5
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 <220>
 <223> Description of Artificial Sequence: DW5_3F

 <400> 5
 attggaacac catggacatt gcacatgac 29

 <210> 6
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 <220>
 <223> Description of Artificial Sequence: DW5_4F

 <400> 6
 aggggtccaat atctccagcc ggaaaccga 29

 <210> 7
 <211> 28
 <212> DNA
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 <220>
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 <400> 7
 gaaaatattt caccgaagtg atcataga 28

 <210> 8
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 <220>

<223> Description of Artificial Sequence: DW5_5F

<400> 8
gggtgccttc tgtctacact tctccag 27

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DW5_5R

<400> 9
aaatgacgag ccaatcccca 20

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: D5-3-1

<400> 10
ttactctgat ttgctgacaa tattcgggtt ttg 33

<210> 11
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: D5-3-2

<400> 11
gtaaaaagggt atgggaaata ttggaagctg tat 33

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: D5-3-3

<400> 12
attgtaacga agtctgttgt tctcatTTTtc tac 33

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: D5-5-1

 <400> 13
 aggagccaga aaagtgtgcg agtc 24

 <210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: D5-5-2

 <400> 14
 caggagaatg acgaaagggtg gaca 24

 <210> 15
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: D5-5-3

 <400> 15
 tggacagaag gcgagaagcg ataa 24

 <210> 16
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: poly T primer
 A1T17

 <400> 16
 ggccacgcgt cgactagtac tttttttttt ttttttt 37

 <210> 17
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
D5WKPN-F

<400> 17
atcgggtacca agcagaagaa gaaaatggcg gag 33

<210> 18
<211> 37
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer
D5BAM-5

<400> 18
atcgggatccg catttttggt ttggctcggt cttttga 37

<210> 19
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signature
sequence 1

<220>
<221> SITE
<222> (3)
<223> Xaa is a variable residue

<220>
<221> SITE
<222> (9)..(10)
<223> Xaa is a variable residue

<400> 19
Leu Leu Xaa Ser Gly Trp Trp Gly Xaa Xaa Arg His
1 5 10

<210> 20
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signature
sequence 2

<220>
 <221> SITE
 <222> (5)..(6)
 <223> Xaa is a variable residue

<400> 20
 Glu Phe Gly Gly Xaa Xaa Gly
 1 5

<210> 21
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: signature
 sequence 3

<400> 21
 Gly Arg Cys Leu Ile Trp Gly Arg Lys
 1 5

<210> 22
 <211> 426
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: LBR-HUMAN

<400> 22
 Lys Glu Leu Ala Val Arg Thr Phe Glu Val Thr Pro Ile Arg Ala Lys
 1 5 10 15
 Asp Leu Glu Phe Gly Gly Val Pro Gly Val Phe Leu Ile Met Phe Gly
 20 25 30
 Leu Pro Val Phe Leu Phe Leu Leu Leu Leu Met Cys Lys Gln Lys Asp
 35 40 45
 Pro Ser Leu Leu Asn Phe Pro Pro Pro Leu Pro Ala Leu Tyr Glu Leu
 50 55 60
 Trp Glu Thr Arg Val Phe Gly Val Tyr Leu Leu Trp Phe Leu Ile Gln
 65 70 75 80
 Val Leu Phe Tyr Leu Leu Pro Ile Gly Lys Val Val Glu Gly Thr Pro
 85 90 95
 Leu Ile Asp Gly Arg Arg Leu Lys Tyr Arg Leu Asn Gly Phe Tyr Pro
 100 105 110

Phe Ile Leu Thr Ser Ala Val Ile Gly Thr Ser Leu Phe Gln Gly Val
115 120 125
Glu Phe His Tyr Val Tyr Ser His Phe Leu Gln Phe Ala Leu Ala Ala
130 135 140
Thr Val Phe Cys Val Val Leu Ser Val Tyr Leu Tyr Met Arg Ser Leu
145 150 155 160
Lys Ala Pro Arg Asn Asp Leu Ser Pro Ala Ser Ser Gly Asn Ala Val
165 170 175
Tyr Asp Phe Phe Ile Gly Arg Glu Leu Asn Pro Arg Ile Gly Thr Phe
180 185 190
Asp Leu Lys Tyr Phe Cys Glu Leu Arg Pro Gly Leu Ile Gly Trp Val
195 200 205
Val Ile Asn Leu Val Met Leu Leu Ala Glu Met Lys Ile Gln Asp Arg
210 215 220
Ala Val Pro Ser Leu Ala Met Ile Leu Val Asn Ser Phe Gln Leu Leu
225 230 235 240
Tyr Val Val Asp Ala Leu Trp Asn Glu Glu Ala Leu Leu Thr Thr Met
245 250 255
Asp Ile Ile His Asp Gly Phe Gly Phe Met Leu Ala Phe Gly Asp Leu
260 265 270
Val Trp Val Pro Phe Ile Tyr Ser Phe Gln Ala Phe Tyr Leu Val Ser
275 280 285
His Pro Asn Glu Val Ser Trp Pro Met Ala Ser Leu Ile Ile Val Leu
290 295 300
Lys Leu Cys Gly Tyr Val Ile Phe Arg Gly Ala Asn Ser Gln Lys Asn
305 310 315 320
Ala Phe Arg Lys Asn Pro Ser Asp Pro Lys Leu Ala His Leu Lys Thr
325 330 335
Ile His Thr Ser Ser Gly Lys Asn Leu Leu Val Ser Gly Trp Trp Gly
340 345 350
Phe Val Arg His Pro Asn Tyr Leu Gly Asp Leu Ile Met Ala Leu Ala
355 360 365
Trp Ser Leu Pro Cys Gly Phe Asn His Ile Leu Pro Tyr Phe Tyr Ile
370 375 380
Ile Tyr Phe Thr Met Leu Leu Val His Arg Glu Ala Arg Asp Glu Tyr
385 390 395 400

His Cys Lys Lys Lys Tyr Gly Val Ala Trp Glu Lys Tyr Cys Gln Arg
405 410 415

Val Pro Tyr Arg Ile Phe Pro Tyr Ile Tyr
420 425

<210> 23
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: LBR-RAT

<400> 23
Arg Gly Pro Val Pro Leu Gly Thr Phe Gln Val Thr Thr Pro Gln Arg
1 5 10 15
Arg Asp Leu Glu Phe Gly Gly Val Pro Gly Ala Leu Leu Ile Met Leu
20 25 30
Gly Leu Pro Ala Cys Val Phe Leu Leu Leu Leu Gln Cys Ala Gln Lys
35 40 45
Asp Pro Gly Leu Leu Gln Phe Pro Pro Pro Leu Pro Ala Leu Arg Glu
50 55 60
Leu Trp Glu Ala Arg Val Cys Gly Val Tyr Leu Leu Trp Phe Phe Leu
65 70 75 80
Gln Ala Leu Phe Ser Leu Leu Pro Val Gly Lys Val Val Glu Gly Thr
85 90 95
Pro Leu Val Asp Gly Arg Arg Leu Lys Tyr Arg Leu Asn Gly Leu Tyr
100 105 110
Ala Phe Ile Leu Thr Ser Ala Ala Val Gly Thr Ala Val Phe Trp Asp
115 120 125
Ile Glu Leu Tyr Tyr Leu Tyr Thr His Phe Leu Gln Phe Ala Leu Ala
130 135 140
Ala Ile Val Phe Ser Val Val Leu Ser Val Tyr Leu Tyr Ala Arg Ser
145 150 155 160
Leu Lys Val Pro Arg Asp Glu Leu Ser Pro Ala Ser Ser Gly Asn Ala
165 170 175
Val Tyr Asp Phe Phe Ile Gly Arg Glu Leu Asn Pro Arg Ile Gly Ala
180 185 190
Phe Asp Leu Lys Phe Phe Cys Glu Leu Arg Pro Gly Leu Ile Gly Trp
195 200 205

Val Val Ile Asn Leu Val Met Leu Leu Ala Glu Met Lys Val Gln Glu
210 215 220
Arg Ser Ala Pro Ser Leu Ala Met Thr Leu Val Asn Ser Phe Gln Leu
225 230 235 240
Leu Tyr Val Val Asp Ala Leu Trp Phe Glu Glu Ala Leu Leu Thr Thr
245 250 255
Met Asp Ile Ile His Asp Gly Phe Gly Phe Met Leu Ala Phe Gly Asp
260 265 270
Leu Val Trp Val Pro Phe Thr Tyr Ser Leu Gln Ala Phe Tyr Leu Val
275 280 285
Asn His Pro Gln Asp Leu Ser Trp Pro Leu Thr Ser Val Ile Ile Ala
290 295 300
Leu Lys Leu Cys Gly Tyr Val Ile Phe Arg Cys Ala Asn Ser Gln Lys
305 310 315 320
Asn Ala Phe Arg Lys Asn Pro Thr Asp Pro Lys Leu Ala His Leu Lys
325 330 335
Thr Ile Pro Thr Ser Thr Trp Lys Ser Leu Leu Val Ser Gly Trp Trp
340 345 350
Gly Phe Val Arg His Pro Asn Tyr Leu Gly Asp Leu Ile Met Ala Leu
355 360 365
Ala Trp Ser Leu Pro Cys Gly Phe Asn His Ile Leu Pro Tyr Phe Tyr
370 375 380
Val Ile Tyr Phe Thr Ala Leu Leu Ile His Arg Glu Ala Arg Asp Glu
385 390 395 400
His Gln Cys Arg Arg Lys Tyr Gly Leu Ala Trp Glu Lys Tyr Cys Gln
405 410 415
Arg Val Pro Tyr Arg Ile Phe Pro Tyr Ile Tyr
420 425

<210> 24

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: LBR-CHICKEN

<400> 24

Cys Ala Cys Gly Cys Gly Thr Cys Cys Gly Gly Ala Cys Cys Thr Thr
1 5 10 15

Thr Thr Cys Ala Gly Thr Gly Ala Ala Cys Cys Thr Gly Thr Cys Thr
 20 25 30
 Gly Gly Thr Ala Ala Ala Ala Gly Ala Ala Thr Ala Ala Ala Ala Gly
 35 40 45
 Ala Thr Gly Gly Cys Gly Gly Ala Cys Ala Ala Gly Ala Thr Thr Ala
 50 55 60
 Ala Ala Ala Cys Ala Cys Cys Ala Cys Gly Thr Ala Cys Cys Ala Gly
 65 70 75 80
 Thr Gly Ala Ala Thr Thr Gly Gly Ala Gly Thr Thr Cys Gly Gly Ala
 85 90 95
 Gly Gly Ala Cys Cys Ala Cys Thr Gly Gly Gly Ala Gly Cys Cys Cys
 100 105 110
 Thr Ala Cys Thr Gly Thr Thr Ala Cys Thr Cys Thr Thr Thr Gly Thr
 115 120 125
 Ala Ala Thr Gly Cys Cys Gly Gly Gly Ala Ala Cys Ala Gly Thr Cys
 130 135 140
 Thr Thr Gly Thr Ala Thr Cys Thr Thr Cys Thr Gly Gly Thr Gly Ala
 145 150 155 160
 Cys Gly Thr Gly Thr Ala Ala Cys Ala Cys Ala Gly Ala Thr Gly Ala
 165 170 175
 Cys Gly Cys Cys Ala Gly Thr Gly Thr Thr Thr Thr Gly Cys Gly Thr
 180 185 190
 Gly Thr Gly Cys Cys Gly Gly Gly Thr Cys Cys Cys Thr Thr Thr Cys
 195 200 205
 Cys Cys Thr Cys Thr Thr Thr Gly Gly Ala Cys Ala Cys Thr Thr Thr
 210 215 220
 Gly Thr Gly Gly Gly Ala Cys Cys Cys Thr Thr Cys Thr Gly Cys Thr
 225 230 235 240
 Gly Thr Gly Ala Thr Cys Thr Thr Ala Cys Thr Gly Cys Thr Thr Gly
 245 250 255
 Cys Ala Thr Gly Gly Gly Thr Gly Thr Cys Thr Cys Thr Gly Cys Ala
 260 265 270
 Gly Gly Cys Thr Gly Thr Gly Cys Thr Gly Cys Ala Thr Ala Thr Thr
 275 280 285
 Cys Thr Gly Cys Cys Thr Ala Thr Thr Gly Gly Ala Ala Ala Gly Gly
 290 295 300

Thr Ala Ala Cys Cys Gly Ala Ala Gly Gly Ala Ala Thr Thr Ala Cys
 305 310 315 320
 Thr Thr Thr Ala Ala Gly Ala Gly Ala Cys Ala Ala Cys Ala Cys Thr
 325 330 335
 Cys Gly Thr Cys Thr Gly Ala Ala Gly Thr Ala Cys Ala Gly Ala Ala
 340 345 350
 Thr Thr Ala Ala Cys Gly Cys Ala Thr Thr Ala Cys Ala Ala Gly Cys
 355 360 365
 Cys Ala Thr Gly Ala Thr Gly Gly Thr Gly Ala Cys Thr Gly Cys Gly
 370 375 380
 Cys Thr Cys Cys Thr Ala Gly Thr Gly Gly Gly Gly Gly Gly Ala Gly
 385 390 395 400
 Cys Ala Gly Thr Gly Ala Thr Gly Thr Thr Thr Gly Gly Gly Thr Thr
 405 410 415
 Cys Cys Cys Ala Thr Thr Cys Thr Cys Cys Thr Ala Thr Gly Thr Thr
 420 425 430
 Thr Ala Thr Gly Ala Thr Cys Ala Thr Thr Thr Cys Cys Thr Gly Cys
 435 440 445
 Ala Ala Cys Thr Gly Gly Cys Ala Gly Thr Gly Gly Cys Thr Gly Cys
 450 455 460
 Cys Gly Cys Ala Thr Thr Thr Ala Thr Ala Gly Cys Thr Cys Thr Ala
 465 470 475 480
 Gly Thr Thr Cys Thr Cys Ala Gly Cys Ala Thr Cys Thr Thr Thr Cys
 485 490 495
 Thr Cys Thr Ala Thr Gly Cys Cys Ala Ala Gly Thr Cys Cys Cys Thr
 500 505 510
 Thr Gly Cys Ala Gly Cys Thr Cys Cys Thr Gly Ala Ala Thr Cys Ala
 515 520 525
 Gly Cys Gly Cys Thr Gly Gly Cys Ala Cys Cys Gly Gly Gly Ala Gly
 530 535 540
 Gly Gly Ala Ala Thr Thr Cys Ala Gly Gly Thr Ala Ala Cys Cys Cys
 545 550 555 560
 Ala Cys Thr Gly Thr Ala Thr Gly Ala Thr Thr Thr Cys Thr Thr Thr
 565 570 575
 Ala Thr Thr Gly Gly Ala Cys Ala Thr
 580 585

<210> 25
 <211> 424
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: S14R-YEAST

<400> 25
 Met Ala Lys Gly Ala Val Lys Lys Glu Lys Phe Glu Tyr Glu Phe Phe
 1 5 10 15
 Gly Pro Ile Gly Ala Leu Gly Val Thr Val Leu Thr Thr Val Val Ser
 20 25 30
 Phe Gly Ser Phe Tyr Ile Cys Asn Glu Glu Gly Cys Pro Ala Lys Phe
 35 40 45
 Ser Lys Ile Ser His Ile Phe Lys Lys Thr Pro Leu Phe Asp Gln Lys
 50 55 60
 Ser Leu Ile Leu Tyr Leu Leu Trp Phe Ser Thr Leu Thr Leu Leu Trp
 65 70 75 80
 Lys Cys Thr Asn Gly Lys Trp Ala Lys Gly Thr Pro Ile Asp Asp Lys
 85 90 95
 Gly Thr Arg Leu Leu Tyr Lys Ile Asn Gly Phe Asn Ser Ala Cys Leu
 100 105 110
 Ile Leu Gly Val Val Cys Thr Ser Ile Tyr Leu Leu Gly Ala Ser Cys
 115 120 125
 Met Glu Phe Ile Trp Asp Asn Phe Leu Gln Leu Met Phe Ala Ala Tyr
 130 135 140
 Val Phe Ser Val Val Leu Cys Thr Phe Cys Tyr Val Gln Ser Phe Phe
 145 150 155 160
 Gly Lys Gln Gln Leu Ala Lys Gly Gly Thr Ser Gly Asn Ile Leu Phe
 165 170 175
 Asp Trp Phe Ile Gly Arg Ser Leu Asn Pro Arg Ile Gly Asn Phe Asp
 180 185 190
 Ile Lys Cys Phe Cys Glu Leu Arg Pro Gly Leu Ile Leu Trp Val Val
 195 200 205
 Phe Asp Ile Ala Phe Ala Cys His Gln Tyr Leu Val Leu Gly Gly Arg
 210 215 220
 Ile Thr Asp Ser Met Val Leu Val Ile Ile Phe His Thr Trp Tyr Val
 225 230 235 240

Leu Asp Ser Leu Ile Asn Glu Ser Ala Val Leu Thr Thr Met Asp Ile
 245 250 255
 Thr Thr Asp Gly Phe Gly Tyr Met Leu Ser Phe Gly Asp Leu Val Trp
 260 265 270
 Val Pro Phe Leu Tyr Ser Leu Gln Ala Arg Tyr Leu Ala Phe His Pro
 275 280 285
 Val Asp Leu Gly Leu Val Lys Thr Leu Ala Ile Leu Cys Leu Gln Phe
 290 295 300
 Leu Gly Tyr Tyr Ile Phe Arg Gly Ala Asn Gly Gln Lys Asn Arg Phe
 305 310 315 320
 Arg Ser Asn Pro Asn Asp Pro Lys Leu Lys His Leu Lys Phe Ile Gln
 325 330 335
 Thr Lys Arg Gly Thr Lys Leu Leu Thr Ser Gly Trp Trp Gly Met Ala
 340 345 350
 Arg His Ile Asn Tyr Phe Gly Asp Trp Ile Met Ala Trp Ala Trp Cys
 355 360 365
 Leu Pro Ala Gly Phe Gly Ser Pro Ile Pro Tyr Phe Tyr Val Ala Tyr
 370 375 380
 Phe Gly Val Leu Leu Val His Arg Asn Ala Arg Asp Asp His Lys Cys
 385 390 395 400
 Arg Val Lys Tyr Gly Glu Asp Trp Glu Lys Tyr Cys Lys Ala Val Lys
 405 410 415
 Tyr Arg Ile Ile Pro Tyr Val Tyr
 420

<210> 26

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: S7R-HUMAN

<400> 26

Met Ala Ala Lys Leu Gln Pro Asn Ile Pro Lys Ala Lys Ser Leu Asp
 1 5 10 15
 Gly Val Thr Asn Asp Arg Thr Ala Ser Gln Gly Gln Trp Gly Arg Ala
 20 25 30
 Trp Glu Val Asp Trp Phe Ser Leu Ala Ser Val Ile Phe Leu Leu Leu
 35 40 45

Phe Ala Pro Phe Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr
50 55 60
Ser Cys Ala Leu Thr Gly Pro Val Val Asp Ile Val Thr Gly His Ala
65 70 75 80
Arg Leu Ser Asp Ile Trp Ala Lys Thr Pro Pro Ile Thr Arg Lys Ala
85 90 95
Ala Gln Leu Tyr Thr Leu Trp Val Thr Phe Gln Val Leu Leu Tyr Thr
100 105 110
Ser Leu Pro Asp Phe Cys His Lys Phe Leu Pro Gly Tyr Val Gly Gly
115 120 125
Ile Gln Glu Gly Ala Val Thr Pro Ala Gly Val Val Asn Lys Tyr Gln
130 135 140
Ile Asn Gly Leu Gln Ala Trp Leu Leu Thr His Leu Leu Trp Phe Ala
145 150 155 160
Asn Ala His Leu Leu Ser Trp Phe Ser Pro Thr Ile Ile Phe Asp Asn
165 170 175
Trp Ile Pro Leu Leu Trp Cys Ala Asn Ile Leu Gly Tyr Ala Val Ser
180 185 190
Thr Phe Ala Met Val Lys Gly Tyr Phe Phe Pro Thr Ser Ala Arg Asp
195 200 205
Cys Lys Phe Thr Gly Asn Phe Phe Tyr Asn Tyr Met Met Gly Ile Glu
210 215 220
Phe Asn Pro Arg Ile Gly Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn
225 230 235 240
Gly Arg Pro Gly Ile Val Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala
245 250 255
Ala Lys Gln Arg Glu Leu His Ser His Val Thr Asn Ala Met Val Leu
260 265 270
Val Asn Val Leu Gln Ala Ile Tyr Val Ile Asp Phe Phe Trp Asn Glu
275 280 285
Thr Trp Tyr Leu Lys Thr Ile Asp Ile Cys His Asp His Phe Gly Trp
290 295 300
Tyr Leu Gly Trp Gly Asp Cys Val Trp Leu Pro Tyr Leu Tyr Thr Leu
305 310 315 320
Gln Gly Leu Tyr Leu Val Tyr His Pro Val Gln Leu Ser Thr Pro His
325 330 335

Ala Val Gly Val Leu Leu Leu Gly Leu Val Gly Tyr Tyr Ile Phe Arg
340 345 350

Val Ala Asn His Gln Lys Asp Leu Phe Arg Arg Thr Asp Gly Arg Cys
355 360 365

Leu Ile Trp Gly Arg Lys Pro Lys Val Ile Glu Cys Ser Tyr Thr Ser
370 375 380

Ala Asp Gly Gln Arg His His Ser Lys Leu Leu Val Ser Gly Phe Trp
385 390 395 400

Gly Val Ala Arg His Phe Asn Tyr Val Gly Asp Leu Met Gly Ser Leu
405 410 415

Ala Tyr Cys Leu Ala Cys Gly Gly Gly His Leu Leu Pro Tyr Phe Tyr
420 425 430

Ile Ile Tyr Met Ala Ile Leu Leu Thr His Arg Cys Leu Arg Asp Glu
435 440 445

His Arg Cys Ala Ser Lys Tyr Gly Arg Asp Trp Glu Arg Tyr Thr Ala
450 455 460

Ala Val Pro Tyr Arg Leu Leu Pro Gly Ile Phe
465 470 475

<210> 27
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: S7R-RAT

<400> 27
Met Ala Ser Lys Ser Gln His Asn Ala Pro Lys Val Lys Ser Pro Asn
1 5 10 15

Gly Lys Ala Gly Ser Gln Gly Gln Trp Gly Arg Ala Trp Glu Val Asp
20 25 30

Trp Phe Ser Leu Ala Ser Ile Ile Phe Leu Leu Leu Phe Ala Pro Phe
35 40 45

Ile Val Tyr Tyr Phe Ile Met Ala Cys Asp Gln Tyr Ser Cys Ser Leu
50 55 60

Thr Ala Pro Ala Leu Asp Ile Ala Thr Gly His Ala Ser Leu Ala Asp
65 70 75 80

Ile Trp Ala Lys Thr Pro Pro Val Thr Ala Lys Ala Ala Gln Leu Tyr
85 90 95

Ala Leu Trp Val Ser Phe Gln Val Leu Leu Tyr Ser Trp Leu Pro Asp
 100 105 110
 Phe Cys His Arg Phe Leu Pro Gly Tyr Val Gly Gly Val Gln Glu Gly
 115 120 125
 Ala Ile Thr Pro Ala Gly Val Val Asn Lys Tyr Glu Val Asn Gly Leu
 130 135 140
 Gln Ala Trp Leu Ile Thr His Ile Leu Trp Phe Val Asn Ala Tyr Leu
 145 150 155 160
 Leu Ser Trp Phe Ser Pro Thr Ile Ile Phe Asp Asn Trp Ile Pro Leu
 165 170 175
 Leu Trp Cys Ala Asn Ile Leu Gly Tyr Ala Val Ser Thr Phe Ala Met
 180 185 190
 Ile Lys Gly Tyr Leu Phe Pro Thr Ser Ala Glu Asp Cys Lys Phe Thr
 195 200 205
 Gly Asn Phe Phe Tyr Asn Tyr Met Met Gly Ile Glu Phe Asn Pro Arg
 210 215 220
 Ile Gly Lys Trp Phe Asp Phe Lys Leu Phe Phe Asn Gly Arg Pro Gly
 225 230 235 240
 Ile Val Ala Trp Thr Leu Ile Asn Leu Ser Phe Ala Ala Lys Gln Gln
 245 250 255
 Glu Leu Tyr Gly His Val Thr Asn Ser Met Ile Leu Val Asn Val Leu
 260 265 270
 Gln Ala Ile Tyr Val Leu Asp Phe Phe Trp Asn Glu Thr Trp Tyr Leu
 275 280 285
 Lys Thr Ile Asp Ile Cys His Asp His Phe Gly Trp Tyr Leu Gly Trp
 290 295 300
 Gly Asp Cys Val Trp Leu Pro Tyr Leu Tyr Thr Leu Gln Gly Leu Tyr
 305 310 315 320
 Leu Val Tyr His Pro Val Gln Leu Ser Thr Pro Asn Ala Leu Gly Ile
 325 330 335
 Leu Leu Leu Gly Leu Val Gly Tyr Tyr Ile Phe Arg Met Thr Asn His
 340 345 350
 Gln Lys Asp Leu Phe Arg Arg Thr Asp Gly Arg Cys Leu Ile Trp Gly
 355 360 365
 Lys Lys Pro Lys Ala Ile Glu Cys Ser Tyr Thr Ser Ala Asp Gly Leu
 370 375 380

Lys His His Ser Lys Leu Leu Val Ser Gly Phe Trp Gly Val Ala Arg
 385 390 395 400
 His Phe Asn Tyr Thr Gly Asp Leu Met Gly Ser Leu Ala Tyr Cys Leu
 405 410 415
 Ala Cys Gly Gly Gly His Leu Leu Pro Tyr Phe Tyr Ile Ile Tyr Met
 420 425 430
 Thr Ile Leu Leu Thr His Arg Cys Leu Arg Asp Glu His Arg Cys Ala
 435 440 445
 Asn Lys Tyr Gly Arg Asp Trp Glu Arg Tyr Thr Ala Ala Val Pro Tyr
 450 455 460
 Arg Leu Leu Pro Gly Ile Phe
 465 470

<210> 28
 <211> 4880
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (671)..(757)
 <223> dwf5

<220>
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 <222> (1050)..(1271)
 <223> dwf5

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 <222> (1340)..(1396)
 <223> dwf5

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 <222> (1505)..(1606)
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 <222> (2174)..(2287)
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<222> (2776) .. (2874)
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<222> (3982) .. (4047)
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<400> 28
aacttgctct tcttccacaa cacgatctcc tctttccggc tgctacgatt tcgtttaagg 60

atgttgattc gtcgaataaa atctgttcct ttctatcatc atcatcatca ctaggcacta 120

attgcatctc ttaaacatac taaaatttct ggaaatgaaa aaaaactgag aaacgcaaaa 180

gaattcaaca cagcatcaga aaactagatc taggtttcgc cgggagttac caaaaacatt 240

agaaaaaatc gatacttaca cgaattcaac caattctgga gaattttctt ccaaggcaag 300

ccattgcttg cgagtaagaa gaaattggta aactatgact gcgaatcaga gtgaagagaa 360

tttgattttg ttagtctcga ttcatcacta tgtgttgaat acagagatga cgaagatctt 420

ttgaggggtg agagagaaga agctaagaag attgggatca atcaaaaacg atggcgaaga 480

aaagtctcaa gggtaaaatt ggaattagaa aaaacatgtg gagagcacgt gacacgtggg 540

aac acc atc ctg atg ctg gtg tat gtc aca aaa ttc ttc tgg tgg gaa 2504
 Asn Thr Ile Leu Met Leu Val Tyr Val Thr Lys Phe Phe Trp Trp Glu
 230 235 240 245

gct ggt tat tgg aac acc atg gac att gca cat gac cga ggt 2546
 Ala Gly Tyr Trp Asn Thr Met Asp Ile Ala His Asp Arg Gly
 250 255

atgcttctgg tacatatata aaattttatat catcacatcc tcatataggg tacaaggaaa 2606
 gaaagccagt agtaataaca aaagtttctc tactgtttgg ctataatttc cttgccagtt 2666
 ctgtttatat ggctaaggca gcagcatatt attcagatta ttgttactgg ctttaacaca 2726
 tgaacttaag cttacttttc aatgctttat aatttatgat tcttcagct gga ttc tat 2784
 Gly Phe Tyr
 260

ata tgc tgg ggt tgt cta gtg tgg gtg cct tct gtc tac act tct cca 2832
 Ile Cys Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr Thr Ser Pro
 265 270 275

ggc atg tac ctt gtg aac cac ccc gtc gaa ctc gga act cag 2874
 Gly Met Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr Gln
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ggccaatgtg	agtttccaga	tttttaggaa	acaagggtag	atttaaagct	acaaaatcat	997
athtagtgag	ttttaagtaa	tgctcacaag	tttcatttct	ttatgatgca	ga tgg tac	1055
					Trp Tyr	
					30	
aca atg gtt cat cag gat ggt tct gtt act cag acc ttt ggc ttc ttt	1103					
Thr Met Val His Gln Asp Gly Ser Val Thr Gln Thr Phe Gly Phe Phe						
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tgg gag aat gga gtt caa gga ctt atc aac ata tgg cca aga ccc act	1151					
Trp Glu Asn Gly Val Gln Gly Leu Ile Asn Ile Trp Pro Arg Pro Thr						
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Leu Ile Ala Trp Lys Ile Ile Phe Cys Tyr Gly Ala Phe Glu Ala Ile						
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ctt cag ctg ctt ctg cct ggt aaa aga gtt gag ggt cca ata tct cca	1247					
Leu Gln Leu Leu Leu Pro Gly Lys Arg Val Glu Gly Pro Ile Ser Pro						
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gcc gga aac cga cca gtt tac aag gtatgttcaa ttagtcttgt gtgggtggaag	1301					
Ala Gly Asn Arg Pro Val Tyr Lys						
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tac ttt gtg aca cta gca acc tat ctt ggt ctt tgg tgg taagaaatgt	1406					
Tyr Phe Val Thr Leu Ala Thr Tyr Leu Gly Leu Trp Trp						

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Lys

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att gtg gcg tcg tat act aca aca tct ggt gaa act aaa act agt ctt 3541
Ile Val Ala Ser Tyr Thr Thr Thr Ser Gly Glu Thr Lys Thr Ser Leu
335 340 345 350

ctc tta acg tct gga tgg tgagactatt ctacattata cagttacaac 3589
Leu Leu Thr Ser Gly Trp
355

cataaaaaata gacgttggtc atcatcaatg gctttgaatg tgcagg tgg gga ttg 3644
Trp Gly Leu

gct cgt cat ttc cat tat gtt cct gag atc tta agt gct ttc ttc tgg 3692
Ala Arg His Phe His Tyr Val Pro Glu Ile Leu Ser Ala Phe Phe Trp
360 365 370 375

acc gta ccg gct ctc ttc gat aac gtaaaatact atccatctat ttgctatatt 3746
Thr Val Pro Ala Leu Phe Asp Asn
380

cgaagctctt cttgcaagtg aaacgcactt aacatataaa tcctctttgt ttaaaccag 3805

ttc ttg gca tac ttc tac gtc ata ttt ctc acc ctt ctt ctc ttt gat 3853
Phe Leu Ala Tyr Phe Tyr Val Ile Phe Leu Thr Leu Leu Leu Phe Asp
385 390 395

cga gcc aag aga gac gat gac cga tgc cga tca aaa taa gcaccaaac 3902
Arg Ala Lys Arg Asp Asp Asp Arg Cys Arg Ser Lys
400 405 410

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Glu Asn Gly Val Gln Gly Leu Ile Asn Ile Trp Pro Arg Pro Thr Leu
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Ile Ala Trp Lys Ile Ile Phe Cys Tyr Gly Ala Phe Glu Ala Ile Leu
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Gln Leu Leu Leu Pro Gly Lys Arg Val Glu Gly Pro Ile Ser Pro Ala
85 90 95
Gly Asn Arg Pro Val Tyr Lys Ala Asn Gly Leu Ala Ala Tyr Phe Val
100 105 110
Thr Leu Ala Thr Tyr Leu Gly Leu Trp Trp Phe Gly Ile Phe Asn Pro
115 120 125
Ala Ile Val Tyr Asp His Leu Gly Glu Ile Phe Ser Ala Leu Ile Phe
130 135 140
Gly Ser Phe Ile Phe Cys Val Leu Leu Tyr Ile Lys Gly His Val Ala
145 150 155 160
Pro Ser Ser Ser Asp Ser Gly Ser Cys Gly Asn Leu Ile Ile Asp Phe
165 170 175

Tyr Trp Gly Met Glu Leu Tyr Pro Arg Ile Gly Lys Ser Phe Asp Ile
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 Lys Val Phe Thr Asn Cys Arg Phe Gly Met Met Ser Trp Ala Val Leu
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 Ala Val Thr Tyr Cys Ile Lys Gln Tyr Glu Ile Asn Gly Lys Val Ser
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 Asp Ser Met Leu Val Asn Thr Ile Leu Met Leu Val Tyr Val Thr Lys
 225 230 235 240
 Phe Phe Trp Trp Glu Ala Gly Tyr Trp Asn Thr Met Asp Ile Ala His
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 260 265 270
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 Thr Asn Gly Lys Cys Leu Val Trp Gly Arg Ala Pro Ser Lys Ile Val
 325 330 335
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 Thr Ser Gly Trp Trp Gly Leu Ala Arg His Phe His Tyr Val Pro Glu
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Ser	Pro	Ile	Val	Thr	Tyr	Ala	Ser	Met	Leu	Ser	Leu	Leu	Ala	Phe	Cys	
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Pro	Pro	Phe	Val	Ile	Leu	Leu	Trp	Tyr	Thr	Met	Val	His	Gln	Asp	Gly	
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Ser	Val	Thr	Gln	Thr	Phe	Gly	Phe	Phe	Trp	Glu	Asn	Gly	Val	Gln	Gly	
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ctt	atc	aac	ata	tgg	cca	aga	ccc	act	ttg	att	gct	tgg	aaa	att	ata	247
Leu	Ile	Asn	Ile	Trp	Pro	Arg	Pro	Thr	Leu	Ile	Ala	Trp	Lys	Ile	Ile	
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ttt	tgc	tat	gga	gca	ttt	gaa	gct	att	ctt	cag	ctg	ctt	ctg	cct	ggg	295
Phe	Cys	Tyr	Gly	Ala	Phe	Glu	Ala	Ile	Leu	Gln	Leu	Leu	Leu	Pro	Gly	
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aaa	aga	gtt	gag	ggg	cca	ata	tct	cca	gcc	gga	aac	cga	cca	gtt	tac	343
Lys	Arg	Val	Glu	Gly	Pro	Ile	Ser	Pro	Ala	Gly	Asn	Arg	Pro	Val	Tyr	
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aag	gcc	aat	ggg	ctg	gct	gct	tac	ttt	gtg	aca	cta	gca	acc	tat	ctt	391
Lys	Ala	Asn	Gly	Leu	Ala	Ala	Tyr	Phe	Val	Thr	Leu	Ala	Thr	Tyr	Leu	
	105						110					115				
ggg	ctt	tgg	tgg	ttt	gga	atc	ttc	aac	cct	gca	att	gtc	tat	gat	cac	439
Gly	Leu	Trp	Trp	Phe	Gly	Ile	Phe	Asn	Pro	Ala	Ile	Val	Tyr	Asp	His	
	120				125					130						
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Leu	Gly	Glu	Ile	Phe	Ser	Ala	Leu	Ile	Phe	Gly	Ser	Phe	Ile	Phe	Cys	
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gtt	ttg	ttg	tac	ata	aaa	ggc	cat	gtt	gca	cct	tca	tca	agt	gac	tct	535
Val	Leu	Leu	Tyr	Ile	Lys	Gly	His	Val	Ala	Pro	Ser	Ser	Ser	Asp	Ser	
			155						160					165		
ggg	tca	tgt	ggg	aac	cta	ata	att	gac	ttc	tat	tgg	ggc	atg	gag	ttg	583
Gly	Ser	Cys	Gly	Asn	Leu	Ile	Ile	Asp	Phe	Tyr	Trp	Gly	Met	Glu	Leu	
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tac	cct	cga	att	ggg	aag	agc	ttt	gac	atc	aag	gtg	ttt	act	aat	tgc	631
Tyr	Pro	Arg	Ile	Gly	Lys	Ser	Phe	Asp	Ile	Lys	Val	Phe	Thr	Asn	Cys	
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Arg Phe Gly Met Met Ser Trp Ala Val Leu Ala Val Thr Tyr Cys Ile	
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Lys Gln Tyr Glu Ile Asn Gly Lys Val Ser Asp Ser Met Leu Val Asn	
215 220 225 230	
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Thr Ile Leu Met Leu Val Tyr Val Thr Lys Phe Phe Trp Trp Glu Ala	
235 240 245	
ggt tat tgg aac acc atg gac att gca cat gac cga gct gga ttc tat	823
Gly Tyr Trp Asn Thr Met Asp Ile Ala His Asp Arg Ala Gly Phe Tyr	
250 255 260	
ata tgc tgg ggt tgt cta gtg tgg gtg cct tct gtc tac act tct cca	871
Ile Cys Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr Thr Ser Pro	
265 270 275	
ggc atg tac ctt gtg aac cac ccc gtc gaa ctc gga act cag ttg gca	919
Gly Met Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr Gln Leu Ala	
280 285 290	
ata tac att ctc gtt gca gga att ctg tgc att tac ata aac tat gac	967
Ile Tyr Ile Leu Val Ala Gly Ile Leu Cys Ile Tyr Ile Asn Tyr Asp	
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Cys Asp Arg Gln Arg Gln Glu Phe Arg Arg Thr Asn Gly Lys Cys Leu	
315 320 325	
gtt tgg gga aga gcc ccg tca aag att gtg gcg tcg tat act aca aca	1063
Val Trp Gly Arg Ala Pro Ser Lys Ile Val Ala Ser Tyr Thr Thr Thr	
330 335 340	
tct ggt gaa act aaa act agt ctt ctc tta acg tct gga tgg tgg gga	1111
Ser Gly Glu Thr Lys Thr Ser Leu Leu Leu Thr Ser Gly Trp Trp Gly	
345 350 355	
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Leu Ala Arg His Phe His Tyr Val Pro Glu Ile Leu Ser Ala Phe Phe	
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Trp Thr Val Pro Ala Leu Phe Asp Asn Phe Leu Ala Tyr Phe Tyr Val	
375 380 385 390	
ata ttt ctc acc ctt ctt ctc ttt gat cga gcc aag aga gac gat gac	1255
Ile Phe Leu Thr Leu Leu Leu Phe Asp Arg Ala Lys Arg Asp Asp Asp	
395 400 405	
cga tgc cga tca aag tat ggg aaa tat tgg aag ctg tat tgt gag aaa	1303
Arg Cys Arg Ser Lys Tyr Gly Lys Tyr Trp Lys Leu Tyr Cys Glu Lys	

410 415 420
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 Val Lys Tyr Arg Ile Ile Pro Gly Ile Tyr
 425 430

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 35 40 45
 Glu Asn Gly Val Gln Gly Leu Ile Asn Ile Trp Pro Arg Pro Thr Leu
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 Ile Ala Trp Lys Ile Ile Phe Cys Tyr Gly Ala Phe Glu Ala Ile Leu
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 Gln Leu Leu Leu Pro Gly Lys Arg Val Glu Gly Pro Ile Ser Pro Ala
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 Gly Asn Arg Pro Val Tyr Lys Ala Asn Gly Leu Ala Ala Tyr Phe Val
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 Thr Leu Ala Thr Tyr Leu Gly Leu Trp Trp Phe Gly Ile Phe Asn Pro
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 Ala Ile Val Tyr Asp His Leu Gly Glu Ile Phe Ser Ala Leu Ile Phe
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 Gly Ser Phe Ile Phe Cys Val Leu Leu Tyr Ile Lys Gly His Val Ala
 145 150 155 160
 Pro Ser Ser Ser Asp Ser Gly Ser Cys Gly Asn Leu Ile Ile Asp Phe
 165 170 175
 Tyr Trp Gly Met Glu Leu Tyr Pro Arg Ile Gly Lys Ser Phe Asp Ile
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